

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE GENERAL HOSPITAL CORPORATION  
FRUIT STREET  
BOSTON, MA 02114  
UNITED STATES OF AMERICA

APPLICANT/INVENTOR: de la Monte, Suzanne  
Wands, Jack R.

(ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
(B) STREET: 1100 New York Ave., Suite 600  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,908  
(B) FILING DATE: 26-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0609.437PC01

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600  
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

09964666.092801

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|   |     |
|---|-----|
| TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC | 50  |
| Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys                 |     |
| 1 5 10  |     |
| AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC | 98  |
| Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser |     |
| 15 20 25  |     |
| GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC | 146 |
| Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys |     |
| 30 35 40  |     |
| ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT | 194 |
| Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe |     |
| 45 50 55 60   |     |
| CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC | 242 |
| Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro |     |
| 65 70 75  |     |
| TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC | 290 |
| Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala |     |
| 80 85 90  |     |
| CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG | 338 |
| Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met |     |
| 95 100 105  |     |
| TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC | 386 |
| Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu |     |
| 110 115 120   |     |
| CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT | 434 |
| Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile |     |
| 125 130 135 140   |     |
| TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG | 482 |
| Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val |     |
| 145 150 155   |     |
| CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG | 530 |
| Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys |     |

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|   |     |     |      |
|---|-----|-----|------|
| 160   | 165 | 170 |      |
| CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC<br>His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His<br>175 180 185     |     |     | 578  |
| CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG<br>His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln<br>190 195 200     |     |     | 626  |
| AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC<br>Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly<br>205 210 215 220 |     |     | 674  |
| TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC<br>Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser<br>225 230 235     |     |     | 722  |
| CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT<br>Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe<br>240 245 250     |     |     | 770  |
| TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC<br>Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile<br>255 260 265     |     |     | 818  |
| TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT<br>Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala<br>270 275 280     |     |     | 866  |
| GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT<br>Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys<br>285 290 295 300 |     |     | 914  |
| TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG<br>Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp<br>305 310 315     |     |     | 962  |
| CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC<br>Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe<br>320 325 330     |     |     | 1010 |
| TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA<br>Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro<br>335 340 345     |     |     | 1058 |
| CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT<br>His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr<br>350 355 360     |     |     | 1106 |
| TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT<br>Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg<br>365 370 375                       |     |     | 1159 |
| TCCAAAGTGC TGGGATTACA GGC GTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA  |     |     | 1219 |

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AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT 1279  
 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA 1339  
 TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA 1399  
 GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA 1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile  
 1 5 10 15  
 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala  
 20 25 30  
 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg  
 35 40 45  
 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly  
 50 55 60  
 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala  
 65 70 75 80  
 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu  
 85 90 95  
 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp  
 100 105 110  
 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp  
 115 120 125  
 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu  
 130 135 140  
 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp  
 145 150 155 160  
 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala  
 165 170 175  
 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp  
 180 185 190

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Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser  
 195 200 205  
 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro  
 210 215 220  
 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser  
 225 230 235 240  
 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu  
 245 250 255  
 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly  
 260 265 270  
 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly  
 275 280 285  
 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met  
 290 295 300  
 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly  
 305 310 315 320  
 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser  
 325 330 335  
 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn  
 340 345 350  
 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp  
 355 360 365  
 Ser Gln Thr Pro Asp Leu Arg  
 370 375

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|   |     |
|---|-----|
| TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT  | 60  |
| CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC | 120 |
| AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTGTAGTA | 180 |

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GAGATGGAGT TTAACCTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240  
 TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC 300  
 TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCCTGA TGTGCCCCAA GCTGGTCTCC 360  
 TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGTCAGCC 420  
 GTGCCTGGCC TTTTATTTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT 480  
 GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540  
 TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600  
 TTTATTTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660  
 AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC 720  
 CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTGTAT 780  
 TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840  
 GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC 900  
 CTATTTTTTA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960  
 AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020  
 AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080  
 CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AACTCCTGA CCTCAGGTGA 1140  
 CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200  
 GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260  
 TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320  
 TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380  
 C 1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

09564666-092801

|  |      |
|--|------|
| TTTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT | 60   |
| CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC  | 120  |
| AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT  | 180  |
| AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT  | 240  |
| CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCC GCCTCTGCCT  | 300  |
| GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT  | 360  |
| CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC   | 420  |
| TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT  | 480  |
| GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC  | 540  |
| TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTTTAT | 600  |
| TTTTATTTTT AATTTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG | 660  |
| GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG  | 720  |
| CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT  | 780  |
| AGTAGAGATG GGGTTTCACC ATGTTGCGCA GGTGATGCT AGATCTCTTG ACCTTGTGAT   | 840  |
| CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC  | 900  |
| TATTTTTAAT TTTTGTTTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA  | 960  |
| ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT  | 1020 |
| CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT    | 1080 |
| TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACCTC TGACCTCAGG  | 1140 |
| TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GCGGTGACGC CTCACCCAGC  | 1200 |
| CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG  | 1260 |
| GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACC AGCCAGTCAC    | 1320 |
| ATTTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG  | 1380 |
| AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT                          | 1418 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

09964655-092801

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

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Applicant's or agent's file  
reference number 0609.437PC01

International application  
TBA

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM  
(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 5, line 11.

**B. IDENTIFICATION OF DEPOSIT**

Further deposits are identified on an additional sheet ☐

Name of depositary institution  
AMERICAN TYPE CULTURE COLLECTION

Address of depositary institution (including postal code and country)

12301 Parklawn Drive  
Rockville, Maryland 20852  
United States of America

Date of deposit  
March 16, 1993

Accession Number  
69262

**C. ADDITIONAL INDICATIONS** (leave blank if not applicable)

This information is continued on an additional sheet ☐

Escherichia coli: AD10-7-DH1

**D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE** (if the indications are not for all designated States)

**E. SEPARATE FURNISHING OF INDICATIONS** (leave blank if not applicable)

The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")

For receiving Office use only

☐ This sheet was received with the international application

Authorized officer

For International Bureau use only

☐ This sheet was received by the International Bureau on:

Authorized officer

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne  
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
  - (B) STREET: 1100 New York Ave., Suite 600
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Esmond, Robert W.
  - (B) REGISTRATION NUMBER: 32,893
  - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202-371-2600
  - (B) TELEFAX: 202-371-2540

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1442 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 15..1139
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC  
 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys  
 1 5 10

50

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAT | GGC | GCA | ATC | TCA | GCT | CAC | CGC | AAC | CTC | CGC | CTC | CCG | GGT | TCA | AGC | 98  |
| Asn | Gly | Ala | Ile | Ser | Ala | His | Arg | Asn | Leu | Arg | Leu | Pro | Gly | Ser | Ser |     |
|     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |
| GAT | TCT | CCT | GCC | TCA | GCC | TCC | CCA | GTA | GCT | GGG | ATT | ACA | GGC | ATG | TGC | 146 |
| Asp | Ser | Pro | Ala | Ser | Ala | Ser | Pro | Val | Ala | Gly | Ile | Thr | Gly | Met | Cys |     |
|     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |
| ACC | CAC | GCT | CGG | CTA | ATT | TTG | TAT | TTT | TTT | TTA | GTA | GAG | ATG | GAG | TTT | 194 |
| Thr | His | Ala | Arg | Leu | Ile | Leu | Tyr | Phe | Phe | Leu | Val | Glu | Met | Glu | Phe |     |
|     | 45  |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| CTC | CAT | GTT | GGT | CAG | GCT | GGT | CTC | GAA | CTC | CCG | ACC | TCA | GAT | GAT | CCC | 242 |
| Leu | His | Val | Gly | Gln | Ala | Gly | Leu | Glu | Leu | Pro | Thr | Ser | Asp | Asp | Pro |     |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |
| TCC | GTC | TCG | GCC | TCC | CAA | AGT | GCT | AGA | TAC | AGG | ACT | GGC | CAC | CAT | GCC | 290 |
| Ser | Val | Ser | Ala | Ser | Gln | Ser | Ala | Arg | Tyr | Arg | Thr | Gly | His | His | Ala |     |
|     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |
| CGG | CTC | TGC | CTG | GCT | AAT | TTT | TGT | GGT | AGA | AAC | AGG | GTT | TCA | CTG | ATG | 338 |
| Arg | Leu | Cys | Leu | Ala | Asn | Phe | Cys | Gly | Arg | Asn | Arg | Val | Ser | Leu | Met |     |
|     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |
| TGC | CCA | AGC | TGG | TCT | CCT | GAG | CTC | AAG | CAG | TCC | ACC | TGC | CTC | AGC | CTC | 386 |
| Cys | Pro | Ser | Trp | Ser | Pro | Glu | Leu | Lys | Gln | Ser | Thr | Cys | Leu | Ser | Leu |     |
|     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |
| CCA | AAG | TGC | TGG | GAT | TAC | AGG | CGT | GCA | GCC | GTG | CCT | GGC | CTT | TTT | ATT | 434 |
| Pro | Lys | Cys | Trp | Asp | Tyr | Arg | Arg | Ala | Ala | Val | Pro | Gly | Leu | Phe | Ile |     |
|     | 125 |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |
| TTA | TTT | TTT | TTA | AGA | CAC | AGG | TGT | CCC | ACT | CTT | ACC | CAG | GAT | GAA | GTG | 482 |
| Leu | Phe | Phe | Leu | Arg | His | Arg | Cys | Pro | Thr | Leu | Thr | Gln | Asp | Glu | Val |     |
|     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |
| CAG | TGG | TGT | GAT | CAC | AGC | TCA | CTG | CAG | CCT | TCA | ACT | CCT | GAG | ATC | AAG | 530 |
| Gln | Trp | Cys | Asp | His | Ser | Ser | Leu | Gln | Pro | Ser | Thr | Pro | Glu | Ile | Lys |     |
|     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |
| CAT | CCT | CCT | GCC | TCA | GCC | TCC | CAA | GTA | GCT | GGG | ACC | AAA | GAC | ATG | CAC | 578 |
| His | Pro | Pro | Ala | Ser | Ala | Ser | Gln | Val | Ala | Gly | Thr | Lys | Asp | Met | His |     |
|     |     |     | 175 |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |
| CAC | TAC | ACC | TGG | CTA | ATT | TTT | ATT | TTT | ATT | TTT | AAT | TTT | TTG | AGA | CAG | 626 |
| His | Tyr | Thr | Trp | Leu | Ile | Phe | Ile | Phe | Ile | Phe | Asn | Phe | Leu | Arg | Gln |     |
|     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     |     |
| AGT | CTC | AAC | TCT | GTC | ACC | CAG | GCT | GGA | GTG | CAG | TGG | CGC | AAT | CTT | GGC | 674 |
| Ser | Leu | Asn | Ser | Val | Thr | Gln | Ala | Gly | Val | Gln | Trp | Arg | Asn | Leu | Gly |     |
|     | 205 |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |
| TCA | CTG | CAA | CCT | CTG | CCT | CCC | GGG | TTC | AAG | TTA | TTC | TCC | TGC | CCC | AGC | 722 |
| Ser | Leu | Gln | Pro | Leu | Pro | Pro | Gly | Phe | Lys | Leu | Phe | Ser | Cys | Pro | Ser |     |
|     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |
| CTC | CTG | AGT | AGC | TGG | GAC | TAC | AGG | CGC | CCA | CCA | CGC | CTA | GCT | AAT | TTT | 770 |
| Leu | Leu | Ser | Ser | Trp | Asp | Tyr | Arg | Arg | Pro | Pro | Arg | Leu | Ala | Asn | Phe |     |
|     |     |     |     | 240 |     |     |     | 245 |     |     |     |     | 250 |     |     |     |
| TTT | GTA | TTT | TTA | GTA | GAG | ATG | GGG | TTC | ACC | ATG | TTC | GCC | AGG | TTG | ATC | 818 |
| Phe | Val | Phe | Leu | Val | Glu | Met | Gly | Phe | Thr | Met | Phe | Ala | Arg | Leu | Ile |     |
|     |     | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |
| TTG | ATC | TCT | GGA | CCT | TGT | GAT | CTG | CCT | GCC | TCG | GCC | TCC | CAA | AGT | GCT | 866 |

|            |            |            |            |            |            |      |     |     |     |     |            |            |      |     |     |      |  |
|------------|------------|------------|------------|------------|------------|------|-----|-----|-----|-----|------------|------------|------|-----|-----|------|--|
| Leu        | Ile        | Ser        | Gly        | Pro        | Cys        | Asp  | Leu | Pro | Ala | Ser | Ala        | Ser        | Gln  | Ser | Ala |      |  |
| 270        |            |            |            |            |            | 275  |     |     |     |     | 280        |            |      |     |     |      |  |
| GGG        | ATT        | ACA        | GGC        | GTG        | AGC        | CAC  | CAC | GCC | CGG | CTT | ATT        | TTT        | AAT  | TTT | TGT | 914  |  |
| Gly        | Ile        | Thr        | Gly        | Val        | Ser        | His  | His | Ala | Arg | Leu | Ile        | Phe        | Asn  | Phe | Cys |      |  |
| 285        |            |            |            |            | 290        |      |     |     |     | 295 |            |            |      |     | 300 |      |  |
| TTG        | TTT        | GAA        | ATG        | GAA        | TCT        | CAC  | TCT | GTT | ACC | CAG | GCT        | GGA        | GTG  | CAA | TGG | 962  |  |
| Leu        | Phe        | Glu        | Met        | Glu        | Ser        | His  | Ser | Val | Thr | Gln | Ala        | Gly        | Val  | Gln | Trp |      |  |
|            |            |            |            | 305        |            |      |     |     | 310 |     |            |            |      | 315 |     |      |  |
| CCA        | AAT        | CTC        | GGC        | TCA        | CTG        | CAA  | CCT | CTG | CCT | CCC | GGG        | CTC        | AAG  | CGA | TTC | 1010 |  |
| Pro        | Asn        | Leu        | Gly        | Ser        | Leu        | Gln  | Pro | Leu | Pro | Pro | Gly        | Leu        | Lys  | Arg | Phe |      |  |
|            |            |            | 320        |            |            |      |     | 325 |     |     |            |            | 330  |     |     |      |  |
| TCC        | TGT        | CTC        | AGC        | CTC        | CCA        | AGC  | AGC | TGG | GAT | TAC | GGG        | CAC        | CTG  | CCA | CCA | 1058 |  |
| Ser        | Cys        | Leu        | Ser        | Leu        | Pro        | Ser  | Ser | Trp | Asp | Tyr | Gly        | His        | Leu  | Pro | Pro |      |  |
|            |            | 335        |            |            |            |      | 340 |     |     |     |            | 345        |      |     |     |      |  |
| CAC        | CCC        | GCT        | AAT        | TTT        | TGT        | ATT  | TTC | ATT | AGA | GGC | GGG        | GTT        | TCA  | CCA | TAT | 1106 |  |
| His        | Pro        | Ala        | Asn        | Phe        | Cys        | Ile  | Phe | Ile | Arg | Gly | Gly        | Val        | Ser  | Pro | Tyr |      |  |
|            | 350        |            |            |            |            | 355  |     |     |     |     | 360        |            |      |     |     |      |  |
| TTG        | TCA        | GGC        | TGG        | TCT        | CAA        | ACT  | CCT | GAC | CTC | AGG | TGACCCACCT | GCCTCAGCCT | 1159 |     |     |      |  |
| Leu        | Ser        | Gly        | Trp        | Ser        | Gln        | Thr  | Pro | Asp | Leu | Arg |            |            |      |     |     |      |  |
| 365        |            |            |            |            | 370        |      |     |     | 375 |     |            |            |      |     |     |      |  |
| TCCAAAGTGC | TGGGATTACA | GGCGTGAGCC | ACCTCACCCA | GCCGGCTAAT | TTAGATAAAA | 1219 |     |     |     |     |            |            |      |     |     |      |  |
| AAATATGTAG | CAATGGGGGG | TCTTGCTATG | TTGCCCAGGC | TGGTCTCAAA | CTTCTGGCTT | 1279 |     |     |     |     |            |            |      |     |     |      |  |
| CATGCAATCC | TTCCAAATGA | GCCACAACAC | CCAGCCAGTC | ACATTTTSTA | AACAGTTACA | 1339 |     |     |     |     |            |            |      |     |     |      |  |
| TCTTTATTTT | AGTATACTAG | AAAGTAATAC | AATAAACATG | TCAAACCTGC | AAATTCAGTA | 1399 |     |     |     |     |            |            |      |     |     |      |  |
| GTAACAGAGT | TCTTTTATAA | CTTTTAAACA | AAGCTTTAGA | GCA        |            | 1442 |     |     |     |     |            |            |      |     |     |      |  |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Glu | Phe | Ser | Leu | Leu | Leu | Pro | Arg | Leu | Glu | Cys | Asn | Gly | Ala | Ile |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser | Ala | His | Arg | Asn | Leu | Arg | Leu | Pro | Gly | Ser | Ser | Asp | Ser | Pro | Ala |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Ser | Ala | Ser | Pro | Val | Ala | Gly | Ile | Thr | Gly | Met | Cys | Thr | His | Ala | Arg |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Leu | Ile | Leu | Tyr | Phe | Phe | Leu | Val | Glu | Met | Glu | Phe | Leu | His | Val | Gly |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Gln | Ala | Gly | Leu | Glu | Leu | Pro | Thr | Ser | Asp | Asp | Pro | Ser | Val | Ser | Ala |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Ser | Gln | Ser | Ala | Arg | Tyr | Arg | Thr | Gly | His | His | Ala | Arg | Leu | Cys | Leu |  |  |

| 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Phe | Cys | Gly | Arg | Asn | Arg | Val | Ser | Leu | Met | Cys | Pro | Ser | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Pro | Glu | Leu | Lys | Gln | Ser | Thr | Cys | Leu | Ser | Leu | Pro | Lys | Cys | Trp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Tyr | Arg | Arg | Ala | Ala | Val | Pro | Gly | Leu | Phe | Ile | Leu | Phe | Phe | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | His | Arg | Cys | Pro | Thr | Leu | Thr | Gln | Asp | Glu | Val | Gln | Trp | Cys | Asp |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| His | Ser | Ser | Leu | Gln | Pro | Ser | Thr | Pro | Glu | Ile | Lys | His | Pro | Pro | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Ala | Ser | Gln | Val | Ala | Gly | Thr | Lys | Asp | Met | His | His | Tyr | Thr | Trp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ile | Phe | Ile | Phe | Ile | Phe | Asn | Phe | Leu | Arg | Gln | Ser | Leu | Asn | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Thr | Gln | Ala | Gly | Val | Gln | Trp | Arg | Asn | Leu | Gly | Ser | Leu | Gln | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Pro | Pro | Gly | Phe | Lys | Leu | Phe | Ser | Cys | Pro | Ser | Leu | Leu | Ser | Ser |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Trp | Asp | Tyr | Arg | Arg | Pro | Pro | Arg | Leu | Ala | Asn | Phe | Phe | Val | Phe | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Glu | Met | Gly | Phe | Thr | Met | Phe | Ala | Arg | Leu | Ile | Leu | Ile | Ser | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Cys | Asp | Leu | Pro | Ala | Ser | Ala | Ser | Gln | Ser | Ala | Gly | Ile | Thr | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Ser | His | His | Ala | Arg | Leu | Ile | Phe | Asn | Phe | Cys | Leu | Phe | Glu | Met |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Ser | His | Ser | Val | Thr | Gln | Ala | Gly | Val | Gln | Trp | Pro | Asn | Leu | Gly |
|     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Ser | Leu | Gln | Pro | Leu | Pro | Pro | Gly | Leu | Lys | Arg | Phe | Ser | Cys | Leu | Ser |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Pro | Ser | Ser | Trp | Asp | Tyr | Gly | His | Leu | Pro | Pro | His | Pro | Ala | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Phe | Cys | Ile | Phe | Ile | Arg | Gly | Gly | Val | Ser | Pro | Tyr | Leu | Ser | Gly | Trp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Gln | Thr | Pro | Asp | Leu | Arg |     |     |     |     |     |     |     |     |     |
|     | 370 |     |     |     | 375 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|  |      |
|--|------|
| TTTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT | 60   |
| CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC  | 120  |
| AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA  | 180  |
| GAGATGGAGT TTAACCTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC | 240  |
| TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC  | 300  |
| TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCACTGA TGTGCCCCAA GCTGGTCTCC   | 360  |
| TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCCTCAGCC  | 420  |
| GTGCCTGGCC TTTTATTTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT   | 480  |
| GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC  | 540  |
| TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT  | 600  |
| TTTATTTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC | 660  |
| AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC  | 720  |
| CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTTGTAT  | 780  |
| TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT  | 840  |
| GATCTGCCTG CCTCGGCCCTA CCCAAAGTGC TGGGATTACA GGTCTGTACT CCACGCCGGC | 900  |
| CTATTTTTTAA TTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC  | 960  |
| AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC  | 1020 |
| AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT  | 1080 |
| CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA  | 1140 |
| CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC  | 1200 |
| GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC  | 1260 |
| TCAAACCTTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT | 1320 |
| TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA  | 1380 |
| C  | 1381 |

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| TTTTTTTTTTT | GAGATGGAGT | TTTCGCTCTT | GTTGCCCAGG | CTGGAGTGCA | ATGGCGCAAT  | 60   |
| CTCAGCTCAC  | CGCAACCTCC | GCCTCCCGGG | TTCAAGCGAT | TCTCCTGCCT | CAGCCTCCCC  | 120  |
| AGTAGGCTGG  | GATTACAGGC | ATGTGCACCA | CGCTCGGCTA | ATTTTGTATT | TTTTTTTAGT  | 180  |
| AGAGATGGAG  | TTTCTCCATG | TTGGTCAGGC | TGGTCTCGAA | CTCCGACCTC | AGATGATCCT  | 240  |
| CCCGTCTCGG  | CCTCCCAAAG | TGCTAGATAC | AGGACTGAGC | ACCATGCCCC | GCCTCTGCCT  | 300  |
| GGCTAATTTT  | TGTGGTAGAA | ACAGGGTTTC | ACTGATGTGC | CCAAGCTGGT | CTCCTGAGCT  | 360  |
| CAAGCAGTCC  | ACCTGCCTCA | GCCTCCCAA  | GTGCTGGGAT | TACAGGCGTG | CAGCCGTGCC  | 420  |
| TGGCCTTTTT  | ATTTTATTTT | TTTAAAGACA | CAGGTGTCCC | ACTCTTACCC | AGGATGAAGT  | 480  |
| GCAGTGGTGT  | GATCACAGCT | CACTGCAGCC | TTCAACTCTG | AGATCAAGCA | TCCTCCTGCC  | 540  |
| TCAGCCTCCC  | AAAGTAGCTG | GGACCAAAGA | CATGCACCAC | TACACCTGGC | TAATTTTTAT  | 600  |
| TTTTATTTTT  | AATTTTTTGA | GACAGAGTCT | CAACTCTGTC | ACCCAGGCTG | GAGTGCAGTG  | 660  |
| GCGCAATCTT  | GGCTCACTGC | AACCTCTGCC | TCCCGGGTTC | AAGTTATTCT | CCTGCCCCAG  | 720  |
| CCTCCTGAGT  | AGCTGGGACT | ACAGGCGCCC | ACCACGCCTA | GCTAATTTTT | TTGTATTTTT  | 780  |
| AGTAGAGATG  | GGGTTTCACC | ATGTTCGCCA | GGTTGATGCT | AGATCTCTTG | ACCTTGTGAT  | 840  |
| CTGCCTGCCT  | CGGCCTCCCA | AAGTGCTGGG | ATTACAGGAC | GTGACGCCCA | CCGCCCCGGC  | 900  |
| TATTTTTTAAT | TTTGTTTTGT | TTGAAATGGA | ATCTCACTCT | GTTACCCAGG | CTGGAGTGCA  | 960  |
| ATGGCCAAAT  | CTCGGCTCAC | TGCAACCTCT | GCCTCCCGGG | CTCAAGCGAT | TCTCCTGTCT  | 1020 |
| CAGCCTCCCA  | AGCAGCTGGG | ATTACGGGCA | CCTGCACCAC | ACCCCGCTAA | TTTTTGTATT  | 1080 |
| TTCATTAGAG  | GCGGGGTTTC | ACCATATTTG | TCAGGCTGGT | CTCAAACTCC | TGACCTCAGG  | 1140 |
| TGACCCACCT  | GCCTCAGCCT | TCCAAAGTGC | TGGGATTACA | GGCGTGACGC | CTCACCACAGC | 1200 |
| CGGCTAATTT  | AGATAAAAAA | ATATGTAGCA | ATGGGGGGTC | TTGCTATGTT | GCCCAGGCTG  | 1260 |
| GTCTCAAACT  | TCTGGCTTCA | TGCAATCCTT | CCAAATGAGC | CACAACACCC | AGCCAGTCAC  | 1320 |
| ATTTTTTAAAC | AGTTACATCT | TTATTTTAGT | ATACTAGAAA | GTGATACGAT | AACATGGCGG  | 1380 |
| AACCTGCAAA  | TTGAGTAGT  | ACAGAGTCTT | TTATAACT   |            |             | 1418 |

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09964565-092801  
T08260-9964565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09564666-092801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

0954566-092801  
108260"99949660